## SEQUENCE LISTING

<110> Gregory, Richard L.

<120> Methods and Compositions for Controlling Dental Caries, and Recombinant SmaA Polypeptides Useful for Same

<130> IU97

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<150> 60/132,312

<151> 1999-05-03

<160> 6

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Streptococcus mutans

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Glu Glu Gln Ser Gly Gly Thr

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Tyr Leu Met Lys Gly Gly Thr

5

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Met Ser Ser Gln Ala Lys Ala Asn Asn Ile Pro

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<212> DNA

<213> Streptococcus mutans

<220>

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## Met Asn Gln Lys Ile Val

•			_	Phe		_			Ala					Lys	gca Ala	881
_			. Asr	_		_		Lys		_		_	Ile	_	att Ilė	929
		Glr													gct Ala	977
	Ser			att Ile							Gly					1025
•				cag Gln 75										_	_	1073
				gaa Glu												1121
				caa Gln					•						_	1169
			_	agt Ser	_	_		-		_						1217
				tcc Ser											_	1265
			Val	gaa Glu 155												1313
		Pro		gtc Val		_	Glu		-							1361
aat	aaa	atg	gtc .	acc	tcg (	gct	cca	gct	aag	gag	act	gag	gca	gaa	caa	1409

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Asn	Ļys	Met 185	Val	Thr	Ser	Ala	Pro 190	Ala	Lys	GIU	THE	195	Ala	Glu	GIN	
aat	gag	aaa	gcg	gtc	aga	gaa	aat	ctt	atg	caa	aga	caa	gct	aag	gct	1457
Asn	Glu	Lys	Ala	Val	Arg	Glu	Asn	Leu	Met	Gln	Arg	Gln	Ala	Lys	Ala	
	200	_				205					210					
gtc	tca	att	cca	tcg	caa	ggc	aat	tat	gtt	ttc	caa	gaa	aca	act	cct	1505
Val	Ser	Ile	Pro	Ser	Gln	Gly	Asn	Tyr	Val	Phe	Gln	Glu	Thr	Thr	Pro	
215					220					225					230	
·																
gta	aaa	aat	gca	gcc	agt	atg	tcc	agc	cca	acc	caa	ttt	aac	ttt	gat	1553
Val	Lys	Asn	Ala	Ala	Ser	Met	Ser	Ser	Pro	Thr	Gln	Phe	Asn	Phe	Asp	
				235					240					245		
aaa	gga	gat	aag	gtt	ttt	tat	gat	aat	gtt	tta	gaa	aca	gat	ggg	cat	1601
Lys	Gly	Asp	Lys	Val	Phe	Tyr	Asp	Asn	Val	Leu	Glu	Ala		Gly	His	•
			250					255					260			
				•												1640
caa	tgg	att	agc	tat	gtg	tct	tac	agt	ggt	att	cgt	cgc	tat	gct	CCL	1649
Gln	Trp	Ile	Ser	Tyr	Val	Ser	Tyr	Ser	Gly	Ile	Arg		Tyr	Ala	Pro	
		265					270					275			-	
																1697
att	gct	gtg	aca	att	gaa	gaa	ttg	aag	caa	aaa	gaa	att	gtt	cag	caa	103,
Ile	Ala	Val	Thr	Ile	Glu	Glu	Leu	Lys	Gln	Lys		TTE	vaı	Gln	GIII	
	280					285					290					
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aat	tta	ccg	gca	caa	gga	acc	tat	cac	בכב	act	aaa	Cay	Cla	agc	Leu	1.15
Asn	Leu	Pro	Ala	Gln		Thr	Tyr	His	Pne		гĀг	GIN	GIII	Ser	310	
295					300					305					310	
											<b>+</b>	car		aca	acq	1793
aaa	atg	aag	cta	aac	tgt	cta	gtc	cga	200	aac	200	7	Pho	aca	Thr	
Lys	Met	Lys	Leu		Cys	Leu	vai	Arg		ASII	261	ALG	FILE	Thr		
				315					320					323		
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Glu	Ile	Thr		Pne	met	TIE	Arg									
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gctc	aaca	at t	cgat	gttg	tc Ca	וכננכ	caat	. gct	.ccaa	igea	auco	,ayy			,-23	
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aaac	aagg	tg a	aggo	gttt	a ta	aggt	gaco	gtt	aagg	gtca	gtga	accat	.aa d	addi	atage	2140

2985

ggtaactate atgtecatet ttattatett ttggataatg gtgaacaaag aggagteggg 2200 gcaacaatga etgaggtga agcaccagag eetgtagaaa caacaggtat cattagcatt 2260 gccaataaga gcagccaagg atttgatgtt ttgattaeta atgetteeag eacteaagae 2320 ataaaaagagg ttttagtgee ggtttggtea gaacaaaacg gacaggaega tattatttgg 2380 tateaagaea etaaacaagg egaaggegtt tataaggtgg eegttaaggt eagtgaacta 2440 aaaaatgaca gtggtaacta taacatteea etttattate geettgtaae tggtgaatta 2500 aaggttgttg gaggaaagae aacgacagta gaageeetta atgaggteaa tetteeagea 2560 caaggaactt atgttteea taataaagtt gaggttaaaa atgaggeeag aacatetagt 2680 gatggacate aatggattag etaeegttee tacagtggta tteegtegtta tattateatt 2740 ggttgaagta aaaaaaggtta ggatgacaaa ateetgaett tttttgtgett tagaattaat 2800 gttggataaa gtgtggagtt tgtggetegaa aaatagcage gattgaatgt gtttataatt 2860 tgattcagae attagtttt atttcaagea aaaaatttga eaaatcaaat caattatatt 2920 acaattettt aaegtttt atttcaagea aaaaaatttga eaaatcaaat caattatatt 2920 acaattettt aaegtataat acaaaaatat atttggaaga tttatteaga tttggaggat 2980

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His Ser Phe Ser Lys Ala Val Tyr His Asn Asp Arg Ser Val Lys Leu 20 25 30

Met Lys Arg Ile Asp Ile Asn His Gln Ala Gln Arg Phe Ser Ile Arg 35 40 45

Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe

Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile Ser Gln Ala Val Ala Asp Lys Ala Ala Thr Gln Thr Thr Leu Thr Glu Thr Pro Gln Val Glu Val Glu Glu Lys Glu Ser Lys Val Asn Ala Pro Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn Pro Thr Ile Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp Ser Ser Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Arg Glu Asn Leu Met Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Asn Val Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly . Ile Arg Arg Tyr Ala Pro Ile Ala Val Thr Ile Glu Glu Leu Lys Gln Lys Glu Ile Val Gln Gln Asn Leu Pro Ala Gln Gly Thr Tyr His Phe 

- Thr Lys Gln Gln Ser Leu Lys Met Lys Leu Asn Cys Leu Val Arg Pro

305 310 315 320

Asn Ser Arg Phe Thr Thr Glu Ile Thr Phe Phe Met Ile Arg Phe 325 330 335

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